



Figure 4a. 158P1D7 amino acid BLAST homology to hypothetical protein FLJ22774.

Identities = 798/798 (100%)

Query: 44 MLINEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI 103
MLINCEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI
Sbjct: 1 MLINEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI 60

Query: 104 EIGAFNGLG L LKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
EIGAFNGLG L LKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61 EIGAFNGLG L LKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTL PYVG FLEHIGRILD LQLEDNKWACN 223
VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTL PYVG FLEHIGRILD LQLEDNKWACN
Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTL PYVG FLEHIGRILD LQLEDNKWACN 180

Query: 224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 283
CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL
Sbjct: 181 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTT SILKLP TKAPGLIPYITK PSTQLPGPYCPIPCNCKVLSPSGL 343
HLAATSSINDSRMSTKTT SILKLP TKAPGLIPYITK PSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241 HLAATSSINDSRMSTKTT SILKLP TKAPGLIPYITK PSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNR IEVLE 403
LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNR IEVLE
Sbjct: 301 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNR IEVLE 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNPM PKLV 463
EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNPM PKLV
Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAI KEILPGTFNPM PKLV 420

Query: 464 LYLN N N L L QVLP P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C 523
LYLN N N L L QVLP P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C
Sbjct: 421 LYLN N N L L QVLP P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C 480

Query: 524 DLVGLQQW IQKLSKNTVTDD I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M 583
DLVGLQQW IQKLSKNTVTDD I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M
Sbjct: 481 DLVGLQQW IQKLSKNTVTDD I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M 540

Query: 584 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV L H R R R R Y K K K Q 643
VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV L H R R R R Y K K K Q
Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLV L H R R R R Y K K K Q 600

Query: 644 VDEQMRDN S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E 703
VDEQMRDN S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E
Sbjct: 601 VDEQMRDN S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E 660

Query: 704 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 763
EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE
Sbjct: 661 EERNEKEGSDAKHLQRSLL EQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

Figure 4b

Query: 824 KANLHAEPDYLEVLEQQT 841 (SEQ ID NO:657)
KANLHAEPDYLEVLEQQT
Sbjct: 781 KANLHAEPDYLEVLEQQT 798 (SEQ ID NO:658)

Figure 5a: Alignment of 158P1D7 with human FLJ22774, CLONE KAIA1575. [Homo sapiens]

Identities = 405/415 (97%), Positives = 405/415 (97%)

```

158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458 (SEQ ID NO:657)
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPM 415 (SEQ ID
              NO:659)

```

Figure 5b: Alignment of 158P1D7 protein with a human protein similar to IGFALS

Identities = 316/864 (36%), Positives = 459/864 (52%)

```

158P1D7:1  MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M L W+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17  MFLWLFLILSALISSTNADSDISV-----EICNVCSVSVENVLYVNCEKVSRYRPNQLK 71

158P1D7:61  VPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADIEIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72  PPWSNFYHLNFQNNFLNLYPNTFLNFHAVSLHLGNNKLQNIIEGGAFLGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVLI LNDN I LP NIF
Sbjct: 132  NNELKILRADTFLGIENLEYLQADYNLIKYIERGAFNKLHLKVLILNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEAICTPSDLYGRLLKETNKQELCPMGTGSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTTSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCNCVK- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312  LHRLVTKPPKTTN---PSKISGIVAGKALSNNRNLQIVSYQTRVPPLTPCPAPCFCKTH 367

```

158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNN 397
S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368 PSDLGLSVNCQEKNIQSMSELIPKPLNAKKLHVNGNSIKDQDVSDFTDFEGLDLLHLGNS 427

158P1D7:398 RIEVLEEGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428 QITVIKGDVFNHNLNLRRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXHI FSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNLLKSLPVYIFSGAPLARLNLRRNKFMYPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQQWIOKLSKNTVTDDILCTSPGHLDDKKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTPLGPIRSPPGGPVPLSILILSVLILTVFVAFCLLVFVLRNRK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHVMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLSEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVMRNVADKEKDLLHVDTRKRLSTIDELDELFP SRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKKSKKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841 (SEQ ID NO:657)
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848 (SEQ ID NO:660)